1   Supplementary Information
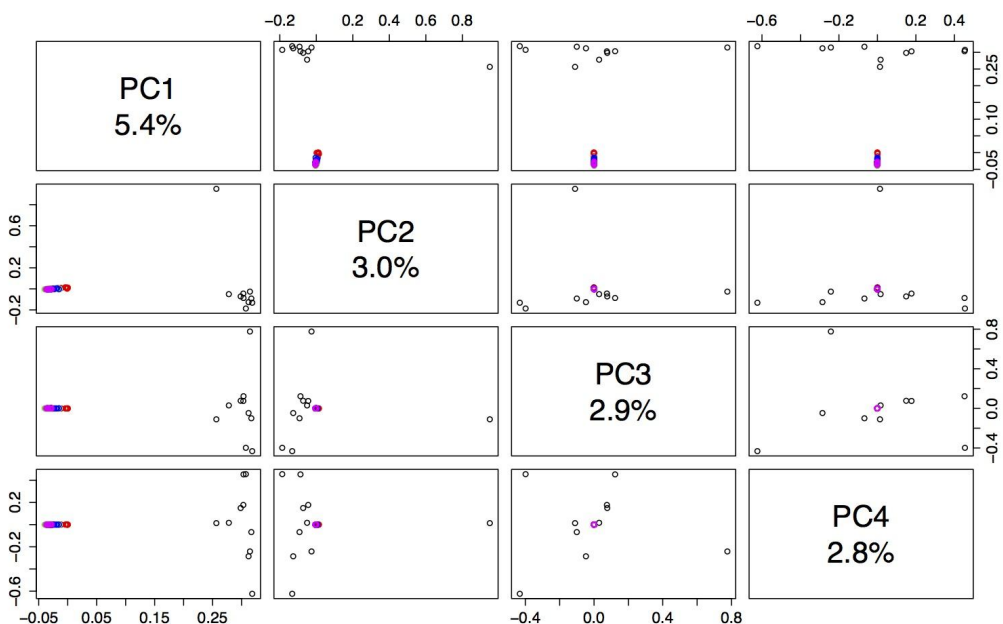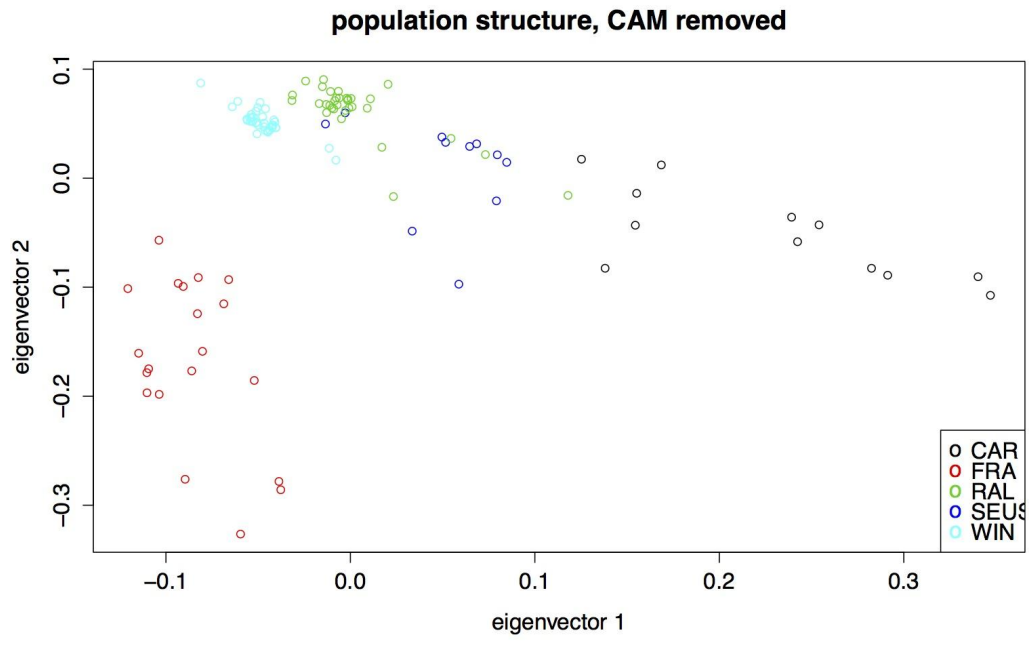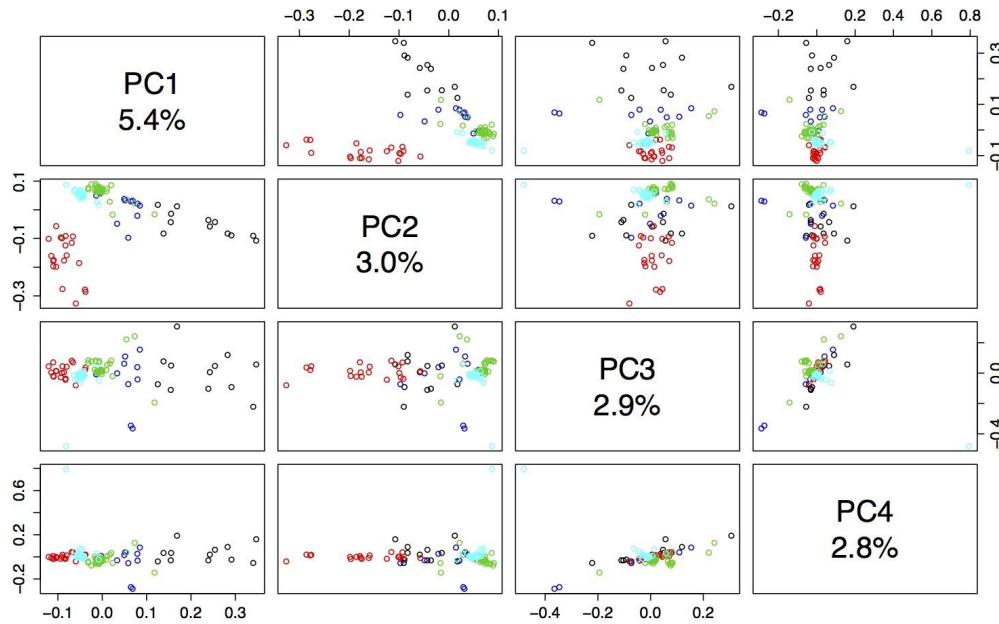2

3
4   FIGURE S1: First four principal components of PCA including populations from
5   Cameroon, Caribbean Islands, France, Raleigh, southeast US, and Winters reveal that
6   most variation explained is within the Cameroon population
7

8

9   FIGURE S2: First and second principal components (eigenvectors) of PCA with the
10   Cameroon population removed, but including populations from Caribbean Islands
11   (CAR), France (FRA), Raleigh (RAL), southeast US (SEU), and Winters (WIN)
12

13
14   FIGURE S3: First four principal components of PCA with the Cameroon population
15   removed, but including populations from Caribbean Islands, France, Raleigh, southeast
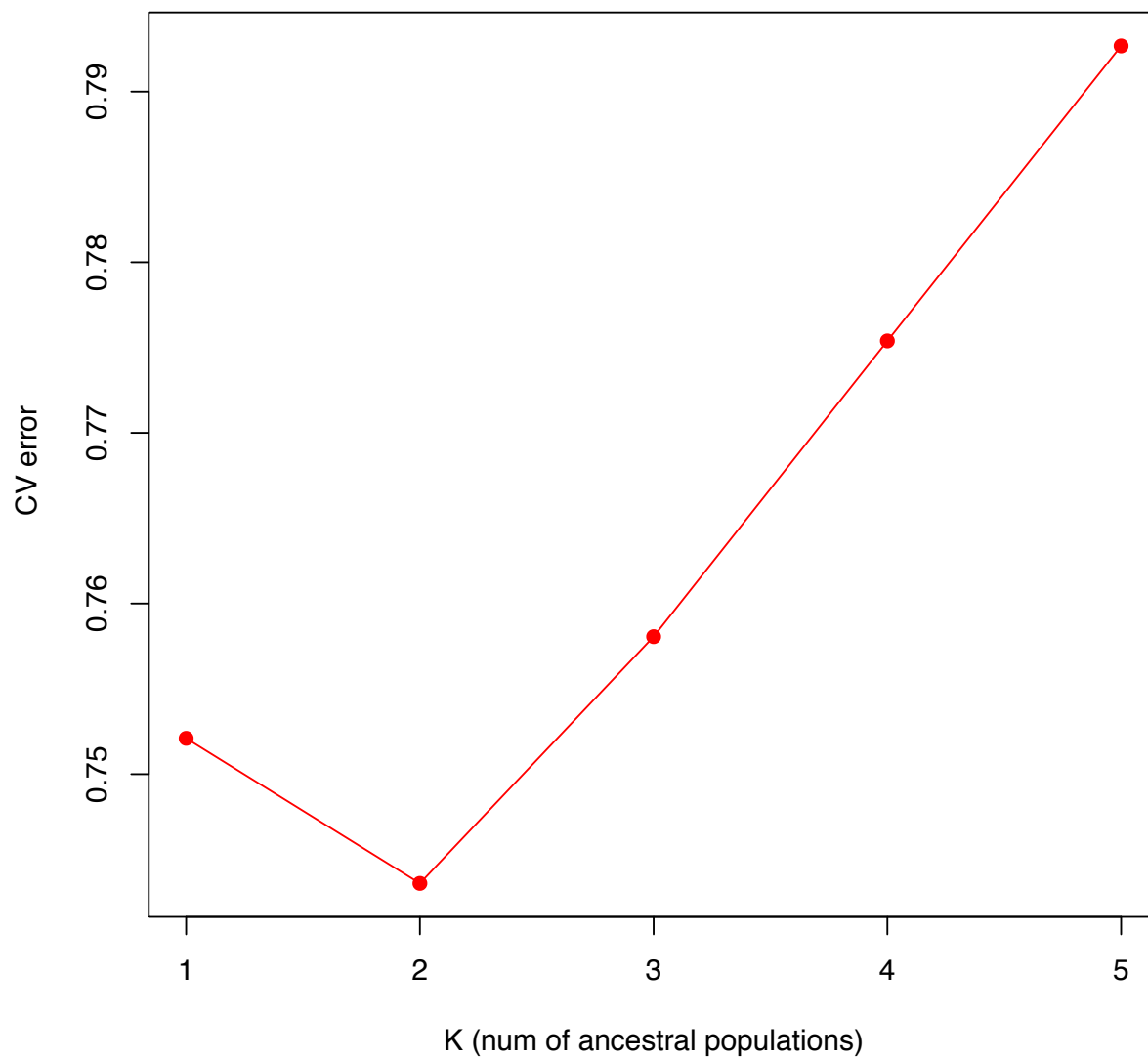16   US, and Winters
17

18
19 FIGURE S4: Cross validation results for ADMIXTURE analysis to determine the optimal
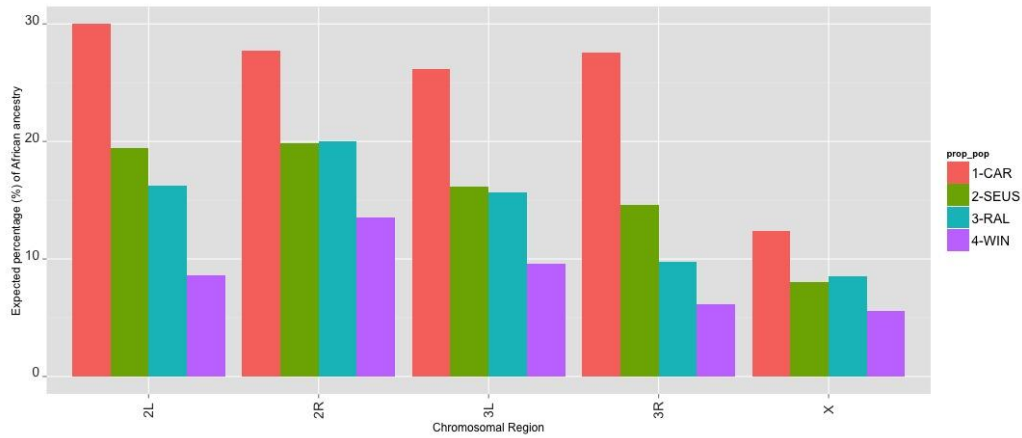20 number of ancestral populations

FIGURE S5: Expected proportion of African ancestry for each population by chromosomal region

CHR 2	FRA	WIN	RAL	SEUS	CAR	CAM
FRA		0.03479	0.04292	0.06273	0.07378	0.17891
WIN	0.03903		0.02220	0.03786	0.04657	0.14145
RAL	0.03795	0.02431		0.02602	0.02985	0.11839
SEUS	0.05114	0.05487	0.03238		0.03815	0.13094
CAR	0.07435	0.09362	0.05798	0.04345		0.11311
CAM	0.14316	0.15647	0.11718	0.11065	0.09201	

TABLE S1: Average F_{ST} values between populations for chromosome 2 divided by regions 2L (below diagonal) and 2R (above diagonal)

CHR 3	FRA	WIN	RAL	SEUS	CAR	CAM
FRA		0.06091	0.04787	0.05638	0.08436	0.15828
WIN	0.03119		0.02519	0.05181	0.10992	0.19523
RAL	0.03769	0.02126		0.04005	0.08867	0.17283
SEUS	0.05548	0.03855	0.02791		0.05206	0.15105
CAR	0.07135	0.05789	0.03810	0.04468		0.13220
CAM	0.17481	0.16001	0.13335	0.14126	0.11451	

28 TABLE S2: Average F_{ST} values between populations for chromosome 3 divided by
29 regions 3L (below diagonal) and 3R (above diagonal)
30